Amendments to the Claims

The following list of claims will replace all prior lists of claims in the application.

List of Claims:

1. (Currently Amended) A method for ~~diagosing~~ diagnosing breast cancer in a subject, comprising:

a) providing a plasma sample from the subject, said plasma sample comprising genomic DNA, wherein said genomic DNA comprises a plurality of promoters from different genes;

b) isolating and digesting said genomic DNA with a methylation sensitive restriction enzyme under conditions such that unmethylated CpG islands in said promoters are cleaved while methylated CpG islands in said promoters are not cleaved;

c) contacting said digested genomic DNA with ~~at least five different pairs of~~ gene specific primers, wherein said gene specific primers are configured to hybridize to said genomic DNA and amplify ~~five~~ different promoters from ~~at least five~~ different genes including DAPK, FAS, MCT1, p16, PAX5, THBS, TRANCE, and VHL, and wherein said contacting is under conditions such that fragments of said plurality of promoters comprising uncleaved CpG islands are amplified, while cleaved promoters comprising cleaved CpG islands are not amplified; and

d) detecting the presence or absence of DNA methylation in each of said plurality of promoters based on the amplification, or lack of amplification, of said fragments to generate a methylation profile for said subject, thereby diagnosing breast cancer in the subject.

2. (Previously Presented) The method of claim 1, wherein said method further comprises comparing said methylation profile to one or more standard methylation profiles, wherein

said standard methylation profiles are selected from the group consisting of methylation profiles of non-cancerous samples and methylation profiles of cancerous samples.

3.-24. (Cancelled)

25. (Previously Presented) The method of Claim 1, wherein said methylation-sensitive restriction enzyme comprises Hin6I.

26. (Previously Presented) The method of Claim 1, further comprising the step of i) separating said plasma sample into a control sample and an experimental sample, and ii) adding control nucleic acid to both said control and experimental samples, wherein said control nucleic acid comprises at least one known CpG island that is unmethylated.

27. (Previously Presented) The method of Claim 26, wherein said control sample is not exposed to said digesting and said experimental sample is exposed to said digesting, and wherein both said control and experimental samples are contacted with primers specific for said control nucleic acid under conditions such that a fragment of said control nucleic acid is amplified only if said known CpG island is uncleaved.

28. (Previously Presented) The method of Claim 27, further comprising comparing any fragments amplified in said control and experimental samples to confirm that said digesting in step b) is complete.

29.-30. (Cancelled)

31. (Previously Presented) The method of Claim 1, wherein said digesting is performed to completion.

32.-34. (Cancelled)

35. (New) A method for characterizing ductal breast cancer in a subject, comprising:

a) providing a plasma sample from the subject, said plasma sample comprising genomic DNA, wherein said genomic DNA comprises a plurality of promoters from different genes;

b) isolating and digesting said genomic DNA with a methylation sensitive restriction enzyme under conditions such that unmethylated CpG islands in said promoters are cleaved while methylated CpG islands in said promoters are not cleaved;

c) contacting said digested genomic DNA with gene specific primers, wherein said gene specific primers are configured to hybridize to said genomic DNA and amplify different promoters from different genes including DAPK, FAS, MCT1, p16, PAX5, THBS, TRANCE, and VHL, and wherein said contacting is under conditions such that fragments of said plurality of promoters comprising uncleaved CpG islands are amplified, while cleaved promoters comprising cleaved CpG islands are not amplified; and

d) detecting the presence or absence of DNA methylation in each of said plurality of promoters based on the amplification, or lack of amplification, of said fragments to generate a methylation profile for said subject, thereby characterizing ductal breast cancer in the subject.

36. (New) A method comprising:

a) providing a plasma sample from the subject, said plasma sample comprising genomic DNA, wherein said genomic DNA comprises a plurality of promoters from different genes;

b) isolating and digesting said genomic DNA with a methylation sensitive restriction enzyme under conditions such that unmethylated CpG islands in said promoters are cleaved while methylated CpG islands in said promoters are not cleaved;

c) contacting said digested genomic DNA with gene specific primers, wherein said gene specific primers are configured to hybridize to said genomic DNA and amplify different promoters from different genes including DAPK, FAS, MCT1, p16, PAX5, THBS, TRANCE, and VHL, and wherein said contacting is under conditions such that fragments of said plurality of promoters comprising uncleaved CpG islands are amplified, while cleaved promoters comprising cleaved CpG islands are not amplified; and

d) detecting the presence or absence of DNA methylation in each of said plurality of promoters based on the amplification, or lack of amplification, of said fragments to generate a methylation profile for said subject.